OIPE

```
          RAW SEQUENCE LISTING            DATE: 07/23/2001
          PATENT APPLICATION:  US/09/782,587    TIME: 13:17:25

          Input Set : A:\310011us.app
          Output Set: N:\CRF3\07232001\I782587.raw
```

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 3 <110> APPLICANT: PEDERSEN, ANDERS H.
 4         ANDERSON, KIM V.
 5         BORNAES, CLAUS
 7 <120> TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
 9 <130> FILE REFERENCE: 31-001100US
11 <140> CURRENT APPLICATION NUMBER: 09/782,587
12 <141> CURRENT FILING DATE: 2001-02-12
14 <150> PRIOR APPLICATION NUMBER: PA 2000 00218
15 <151> PRIOR FILING DATE: 2000-02-11
17 <150> PRIOR APPLICATION NUMBER: 60/184,036
18 <151> PRIOR FILING DATE: 2000-02-22
20 <150> PRIOR APPLICATION NUMBER: 60/241,916
21 <151> PRIOR FILING DATE: 2000-10-18
23 <160> NUMBER OF SEQ ID NOS: 19
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 406
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
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34 <222> LOCATION: (6)..(7)
35 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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39 <222> LOCATION: (16)
40 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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43 <221> NAME/KEY: MOD_RES
44 <222> LOCATION: (19)..(20)
45 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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49 <222> LOCATION: (25)..(26)
50 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
52 <220> FEATURE:
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54 <222> LOCATION: (29)
55 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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58 <221> NAME/KEY: MOD_RES
59 <222> LOCATION: (35)
60 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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64   1               5                   10              15
W--> 66 Cys Lys Xaa Xaa Gln Cys Ser Phe Xaa Xaa Ala Arg Xaa Ile Phe Lys
```

Does Not Comply
Corrected Diskette Needed

see item #9 on ERROR Summary Sheet.

All Xaa's Need numeric Identifiers <220> — <223> and explanation of what Xaa is equal to.

RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/782,587   TIME: 13:17:25

Input Set : A:\31001lus.app
Output Set: N:\CRF3\07232001\I782587.raw

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      67                20                25                30
W--> 69 Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
     70          35                40                45
     72 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
     73      50                55                60
     75 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
     76  65                70                75                80
     78 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
     79              85                90                95
     81 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
     82          100               105               110
     84 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
     85          115               120               125
     87 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
     88      130               135               140
     90 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
     91 145               150               155               160
     93 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
     94              165               170               175
     96 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
     97          180               185               190
     99 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
    100          195               200               205
    102 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
    103      210               215               220
    105 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
    106 225               230               235               240
    108 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
    109              245               250               255
    111 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
    112          260               265               270
    114 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
    115          275               280               285
    117 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
    118      290               295               300
    120 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
    121 305               310               315               320
    123 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
    124              325               330               335
    126 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
    127          340               345               350
    129 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
    130          355               360               365
    132 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
    133      370               375               380
    135 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
    136 385               390               395               400
    138 Leu Arg Ala Pro Phe Pro
    139              405
```

RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/782,587   TIME: 13:17:25

Input Set : A:\31001lus.app
Output Set: N:\CRF3\07232001\I782587.raw

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143 <211> LENGTH: 1338
144 <212> TYPE: DNA
145 <213> ORGANISM: Homo sapiens
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (115)..(1332)
151 <400> SEQUENCE: 2
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154 gccgtcttcg tcacccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc   117
155                                                              Ala
156                                                                1
158 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165
159 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
160                 5                   10                  15
162 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213
163 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
164             20                  25                  30
166 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261
167 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
168         35                  40                  45
170 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309
171 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
172 50                  55                  60                  65
174 cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc 357
175 Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
176                 70                  75                  80
178 gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc 405
179 Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
180             85                  90                  95
182 tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc 453
183 Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
184         100                 105                 110
186 tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc 501
187 Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
188     115                 120                 125
190 acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac 549
191 Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn
192 130                 135                 140                 145
194 gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag 597
195 Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys
196                 150                 155                 160
198 ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg 645
199 Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu
200             165                 170                 175
202 tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac 693
203 Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His
204         180                 185                 190
206 tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc 741
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RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/782,587   TIME: 13:17:25

Input Set : A:\310011us.app
Output Set: N:\CRF3\07232001\I782587.raw

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207 Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly
208     195                 200                 205
210 gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg   789
211 Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val
212 210                 215                 220                 225
214 gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac   837
215 Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His
216                 230                 235                 240
218 gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac   885
219 Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His
220                 245                 250                 255
222 gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg   933
223 Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu
224         260                 265                 270
226 gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac   981
227 Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp
228         275                 280                 285
230 cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg   1029
231 Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu
232 290                 295                 300                 305
234 atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc   1077
235 Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro
236                 310                 315                 320
238 aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag   1125
239 Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys
240                 325                 330                 335
242 gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc   1173
243 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
244         340                 345                 350
246 ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc   1221
247 Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
248         355                 360                 365
250 acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag   1269
251 Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
252 370                 375                 380                 385
254 tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg   1317
255 Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
256                 390                 395                 400
258 cgg gcc cct ttc cct tgataa                                        1338
259 Arg Ala Pro Phe Pro
260                 405
263 <210> SEQ ID NO: 3
264 <211> LENGTH: 406
265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <400> SEQUENCE: 3
269 Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu
270   1               5                 10                  15
272 Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
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RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/782,587   TIME: 13:17:25

Input Set : A:\310011us.app
Output Set: N:\CRF3\07232001\I782587.raw

```
273              20                  25                  30
275 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
276          35                  40                  45
278 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
279      50                  55                  60
281 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
282  65                  70                  75                  80
284 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
285                  85                  90                  95
287 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
288              100                 105                 110
290 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
291          115                 120                 125
293 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
294      130                 135                 140
296 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
297 145                 150                 155                 160
299 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
300              165                 170                 175
302 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
303          180                 185                 190
305 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
306          195                 200                 205
308 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
309      210                 215                 220
311 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
312 225                 230                 235                 240
314 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
315              245                 250                 255
317 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
318          260                 265                 270
320 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
321          275                 280                 285
323 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
324      290                 295                 300
326 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
327 305                 310                 315                 320
329 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
330              325                 330                 335
332 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
333          340                 345                 350
335 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
336          355                 360                 365
338 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
339      370                 375                 380
341 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
342 385                 390                 395                 400
344 Leu Arg Ala Pro Phe Pro
345              405
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VERIFICATION SUMMARY   DATE: 07/23/2001
PATENT APPLICATION: US/09/782,587   TIME: 13:17:27
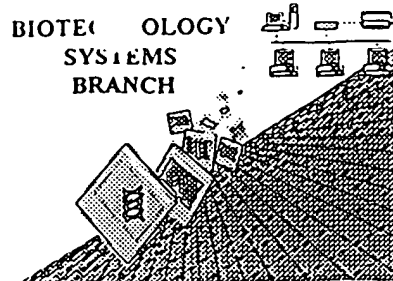
Input Set : **A:\310011us.app**
Output Set: **N:\CRF3\07232001\I782587.raw**

L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/782,587_

Source: _OIPE_

Date Processed by STIC: _7/23/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

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http://www.uspto.gov/web/offices/pac/checker